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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/054,611 /

DATE: 02/07/2002

TIME: 11:09:11

Input Set : N:\Crf3\RULE60\10054611.raw

Output Set: N:\CRF3\02072002\J054611.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Cech, Thomas R.

6 Lingner, Joachim

7 Nakamura, Toru

8 Chapman, Karen B.

9 Morin, Gregg B.

10 Harley, Calvin

11 Andrews, William H.

13 (ii) TITLE OF INVENTION: Novel Telomerase

15 (iii) NUMBER OF SEQUENCES: 225

17 (iv) CORRESPONDENCE ADDRESS:

18 (A) ADDRESSEE: Townsend and Townsend and Crew LLP

19 (B) STREET: Two Embarcadero Center, 8th Floor

20 (C) CITY: San Francisco

21 (D) STATE: California

22 (E) COUNTRY: United States of America

23 (F) ZIP: 94111

25 (v) COMPUTER READABLE FORM:

26 (A) MEDIUM TYPE: Floppy disk

27 (B) COMPUTER: IBM PC compatible

28 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

29 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

31 (vi) CURRENT APPLICATION DATA:

C--> 32 (A) APPLICATION NUMBER: US/10/054,611

C--> 33 (B) FILING DATE: 18-Jan-2002

54 (C) CLASSIFICATION: 536

51 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/854,050

38 (B) FILING DATE:

42 (A) APPLICATION NUMBER: US 08/846,017

43 (B) FILING DATE: 25-APR-1997

47 (A) APPLICATION NUMBER: US 08/844,419

48 (B) FILING DATE: 18-APR-1997

52 (A) APPLICATION NUMBER: US 08/724,643

53 (B) FILING DATE: 01-OCT-1996

56 (viii) ATTORNEY/AGENT INFORMATION:

57 (A) NAME: Apple, Randolph T.

58 (B) REGISTRATION NUMBER: 36,429

59 (C) REFERENCE/DOCKET NUMBER: 015389-002930US

61 (ix) TELECOMMUNICATION INFORMATION:

62 (A) TELEPHONE: (415) 576-0200

63 (B) TELEFAX: (415) 576-0300

ENTERED

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65 (2) INFORMATION FOR SEQ ID NO: 1:

67 (i) SEQUENCE CHARACTERISTICS:

68 (A) LENGTH: 3279 base pairs

69 (B) TYPE: nucleic acid

70 (C) STRANDEDNESS: single

71 (D) TOPOLOGY: linear

73 (ii) MOLECULE TYPE: other nucleic acid

74 (A) DESCRIPTION: /desc = "DNA"

76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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80 TTAATAAGCT CAGATTTTAA ATATTAATTA CAAAACCTAA ATGGAGGTTG ATGTTGATAA      120
82 TCAAGCTGAT AATCATGGCA TTCCTCAGC TCTTAAGACT TGTGAAGAAA TTAAAGAAGC      180
84 TAAACGTTG TACTCTTGGA TCCAGAAAGT TATTAGATGA AGAAATCAAT CTCAAAGTCA      240
86 TTATAAGAT TTAGAAGATA TTAAAATATT TGCGCAGACA AATATTGTTG CTACTCCACG      300
88 AGACTATAAT GAAGAAGATT TTAAAGTTAT TGCAAGAAAA GAAGTATTTT CAACTGGACT      360
90 AATGATCGAA CTTATTGACA AATGCTTAGT TGAACCTCTT TCATCAAGCG ATGTTTCAGA      420
92 TAGACAAAAA CTTCAATGAT TTGGATTTCA ACTTAAGGGA AATCAATTAG CAAAGACCCA      480
94 TTTATTAACA GCTCTTTCAA CTCAAAAGCA GTATTTCTTT CAAGACGAAT GGAACCAAGT      540
96 TAGAGCAATG ATTGGAATG AGCTCTTCCG ACATCTCTAC ACTAAATATT TAATATTCCA      600
98 GCGAACTTCT GAAGGAACTC TTGTTCAATT TTGCGGGAAT AACGTTTTTG ATCATTTGAA      660
100 AGTCAACGAT AAGTTTGACA AAAAGCAAAA AGGTGGAGCA GCAGACATGA ATGAACCTCG      720
102 ATGTTGATCA ACCTGCAAAAT ACAATGTCAA GAATGAGAAA GATCACTTTC TCAACAACAT      780
104 CAACGTGCCG AATTGGAATA ATATGAAATC AAGAACCAGA ATATTTTATT GCACTCATTT      840
106 TAATAGAAAT AACCAATTCT TCAAAAAGCA TGAGTTTGTG AGTAACAAAA ACAATATTTT      900
108 AGCGATGGAC AGAGCTCAGA CGATATTCAC GAATATATTC AGATTTAATA GAATTAGAAA      960
110 GAAGCTAAAA GATAAGGTTA TCGAAAAAAT TGCCTACATG CTTGAGAAAG TCAAAGATTT      1020
112 TAACTTCAAC TACTATTTAA CAAAATCTTG TCCTCTTCCA GAAAATTGGC GGAACCGGAA      1080
114 ACAAAAAATC GAAAACTTGA TAAATAAAAC TAGAGAAGAA AAGTCGAAGT ACTATGAAGA      1140
116 GCTGTTTAGC TACACAACCTG ATAATAAATG CGTCACACAA TTTATTAATG AATTTTTCTA      1200
118 CAATATACTC CCCAAAGACT TTTTGACTGG AAGAAACCGT AAGAATTTTC AAAAGAAAGT      1260
120 TAAGAAATAT GTGGAACATA ACAAGCATGA ACTCATTCAC AAAAATTAT TGCTTGAGAA      1320
122 GATCAATACA AGAGAAATAT CATGGATGCA GGTTGAGACC TCTGCAAAGC ATTTTATTA      1380
124 TTTTGATCAC GAAAACATCT ACGTCTTATG GAAATTGCTC CGATGGATAT TCGAGGATCT      1440
126 CGTCGTCTCG CTGATTAGAT GATTTTTCTA TGTCACCGAG CAACAGAAAA GTTACTCCAA      1500
128 AACCTATTAC TACAGAAAGA ATATTGGGA CGTCATTATG AAAATGTCAA TCGCAGACTT      1560
130 AAAGAAGGAA ACGCTTGCTG AGGTCCAAGA AAAAGAGGTT GAAGAATGGA AAAAGTCGCT      1620
132 TGGATTGCA CCTGGAAAAC TCAGACTAAT ACCGAAGAAA ACTACTTTCC GTCCAATTAT      1680
134 GACTTTCAAT AAGAAGATTG TAAATTCAGA CCGGAAGACT ACAAATTA CTACAAATAC      1740
136 GAAGTTATTG AACTCTCACT TAATGCTTAA GACATTGAAG AATAGAATGT TTAAAGATCC      1800
138 TTTTGGATTG GCTGTTTTTA ACTATGATGA TGTAATGAAA AAGTATGAGG AGTTTGTTTG      1860
140 CAAATGGAAG CAAGTTGGAC AACCAAAACT CTTCTTGCA ACTATGGATA TCGAAAAGTG      1920
142 ATATGATAGT GTAAACAGAG AAAAATATC AACATTCTTA AAACTACTA AATTACTTTC      1980
144 TTCAGATTTT TGGATTATGA CTGCACAAAT TCTAAAGAGA AAGAATAACA TAGTTATCGA      2040
146 TTCGAAAAAC TTTAGAAAGA AAGAAATGAA AGATTATTTT AGACAGAAAT TCCAGAAGAT      2100
148 TGCATTGAA GGAGGACAAT ATCCAACCTT ATTCAGTGTT CTTGAAAATG AACAAAATGA      2160
150 CTAAATGCA AAGAAAACAT TAATTGTTGA AGCAAAGCAA AGAAATTATT TTAAGAAAGA      2220
152 TAACTTACTT CAACCAGTCA TTAATATTTG CCAATATAAT TACATTAAT TTAATGGGAA      2280
154 GTTTTATAAA CAAACAAAAG GAATTCCTCA AGGTCTTTGA GTTTCATCAA TTTTGTCTATC      2340
156 ATTTTATTAT GCAACATTAG AGGAAAGCTC CTTAGGATTC CTTAGAGATG AATCAATGAA      2400

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158 CCCTGAAAAT CCAATGTGTA ATCTTCTAAT GAGACTTACA GATGACTATC TTTTGATTAC 2460
160 AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT ATAAACGTAA GTCGTGAAAA 2520
162 TGGATTTTAAA TTCAATATGA AGAAACTACA GACTAGTTTT CCATTAAGTC CAAGCAAATT 2580
164 TGCAAAATAC GGAATGGATA GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG 2640
166 GATTGGCATC TCAATTGATA TGAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT 2700
168 AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT CAATGTGGCT 2760
170 CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC CATTATTTTA GAAAGACGAT 2820
172 TACAACCGAA GACTTTGCGA ATAAACTCT CAACAAGTTA TTTATATCAG GCGGTTACAA 2880
174 ATACATGCAA TGAGCCAAAG AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG 2940
176 TATGATCGAC TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA 3000
178 CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG ACTTTTTCCT 3060
180 TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA AAGTACATTT TCAACAGAGT 3120
182 TTGCATGATC CTCAAGGCAA AAGAAGCAAA GCTAAAAAGT GACCAATGTC AATCTCTAAT 3180
184 TCAATATGAT GCATAGTCGA CTATTCTAAC TTATTTTGGG AAGTTAATTT TCAATTTTGT 3240
186 TCTTATATAC TGGGGTTTTG GGGTTTTGGG GTTTTGGGG 3279

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188 (2) INFORMATION FOR SEQ ID NO: 2:

190 (i) SEQUENCE CHARACTERISTICS:

191 (A) LENGTH: 1031 amino acids

192 (B) TYPE: amino acid

193 (C) STRANDEDNESS: Not Relevant

W--> 194 (D) TOPOLOGY: Not Relevant

196 (ii) MOLECULE TYPE: protein

198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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200 Met Glu Val Asp Val Asp Asn Gln Ala Asp Asn His Gly Ile His Ser
201 1 5 10 15
203 Ala Leu Lys Thr Cys Glu Glu Ile Lys Glu Ala Lys Thr Leu Tyr Ser
204 20 25 30
206 Trp Ile Gln Lys Val Ile Arg Cys Arg Asn Gln Ser Gln Ser His Tyr
207 35 40 45
209 Lys Asp Leu Glu Asp Ile Lys Ile Phe Ala Gln Thr Asn Ile Val Ala
210 50 55 60
212 Thr Pro Arg Asp Tyr Asn Glu Glu Asp Phe Lys Val Ile Ala Arg Lys
213 65 70 75 80
215 Glu Val Phe Ser Thr Gly Leu Met Ile Glu Leu Ile Asp Lys Cys Leu
216 85 90 95
218 Val Glu Leu Leu Ser Ser Ser Asp Val Ser Asp Arg Gln Lys Leu Gln
219 100 105 110
221 Cys Phe Gly Phe Gln Leu Lys Gly Asn Gln Leu Ala Lys Thr His Leu
222 115 120 125
224 Leu Thr Ala Leu Ser Thr Gln Lys Gln Tyr Phe Phe Gln Asp Glu Trp
225 130 135 140
227 Asn Gln Val Arg Ala Met Ile Gly Asn Glu Leu Phe Arg His Leu Tyr
228 145 150 155 160
230 Thr Lys Tyr Leu Ile Phe Gln Arg Thr Ser Glu Gly Thr Leu Val Gln
231 165 170 175
233 Phe Cys Gly Asn Asn Val Phe Asp His Leu Lys Val Asn Asp Lys Phe
234 180 185 190
236 Asp Lys Lys Gln Lys Gly Gly Ala Ala Asp Met Asn Glu Pro Arg Cys
237 195 200 205

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239   Cys Ser Thr Cys Lys Tyr Asn Val Lys Asn Glu Lys Asp His Phe Leu
240       210                215                220
242   Asn Asn Ile Asn Val Pro Asn Trp Asn Asn Met Lys Ser Arg Thr Arg
243       225                230                235                240
245   Ile Phe Tyr Cys Thr His Phe Asn Arg Asn Asn Gln Phe Phe Lys Lys
246       245                250                255
248   His Glu Phe Val Ser Asn Lys Asn Asn Ile Ser Ala Met Asp Arg Ala
249       260                265                270
251   Gln Thr Ile Phe Thr Asn Ile Phe Arg Phe Asn Arg Ile Arg Lys Lys
252       275                280                285
254   Leu Lys Asp Lys Val Ile Glu Lys Ile Ala Tyr Met Leu Glu Lys Val
255       290                295                300
257   Lys Asp Phe Asn Phe Asn Tyr Tyr Leu Thr Lys Ser Cys Pro Leu Pro
258       305                310                315                320
260   Glu Asn Trp Arg Glu Arg Lys Gln Lys Ile Glu Asn Leu Ile Asn Lys
261       325                330                335
263   Thr Arg Glu Glu Lys Ser Lys Tyr Tyr Glu Glu Leu Phe Ser Tyr Thr
264       340                345                350
266   Thr Asp Asn Lys Cys Val Thr Gln Phe Ile Asn Glu Phe Phe Tyr Asn
267       355                360                365
269   Ile Leu Pro Lys Asp Phe Leu Thr Gly Arg Asn Arg Lys Asn Phe Gln
270       370                375                380
272   Lys Lys Val Lys Lys Tyr Val Glu Leu Asn Lys His Glu Leu Ile His
273       385                390                395                400
275   Lys Asn Leu Leu Leu Glu Lys Ile Asn Thr Arg Glu Ile Ser Trp Met
276       405                410                415
278   Gln Val Glu Thr Ser Ala Lys His Phe Tyr Tyr Phe Asp His Glu Asn
279       420                425                430
281   Ile Tyr Val Leu Trp Lys Leu Leu Arg Trp Ile Phe Glu Asp Leu Val
282       435                440                445
284   Val Ser Leu Ile Arg Cys Phe Phe Tyr Val Thr Glu Gln Gln Lys Ser
285       450                455                460
287   Tyr Ser Lys Thr Tyr Tyr Tyr Arg Lys Asn Ile Trp Asp Val Ile Met
288       465                470                475                480
290   Lys Met Ser Ile Ala Asp Leu Lys Lys Glu Thr Leu Ala Glu Val Gln
291       485                490                495
293   Glu Lys Glu Val Glu Glu Trp Lys Lys Ser Leu Gly Phe Ala Pro Gly
294       500                505                510
296   Lys Leu Arg Leu Ile Pro Lys Lys Thr Thr Phe Arg Pro Ile Met Thr
297       515                520                525
299   Phe Asn Lys Lys Ile Val Asn Ser Asp Arg Lys Thr Thr Lys Leu Thr
300       530                535                540
302   Thr Asn Thr Lys Leu Leu Asn Ser His Leu Met Leu Lys Thr Leu Lys
303       545                550                555                560
305   Asn Arg Met Phe Lys Asp Pro Phe Gly Phe Ala Val Phe Asn Tyr Asp
306       565                570                575
308   Asp Val Met Lys Lys Tyr Glu Glu Phe Val Cys Lys Trp Lys Gln Val
309       580                585                590
311   Gly Gln Pro Lys Leu Phe Phe Ala Thr Met Asp Ile Glu Lys Cys Tyr

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312																
314	Asp	Ser	Val	Asn	Arg	Glu	Lys	Leu	Ser	Thr	Phe	Leu	Lys	Thr	Thr	Lys
315		610					615					620				
317	Leu	Leu	Ser	Ser	Asp	Phe	Trp	Ile	Met	Thr	Ala	Gln	Ile	Leu	Lys	Arg
318		625				630					635					640
320	Lys	Asn	Asn	Ile	Val	Ile	Asp	Ser	Lys	Asn	Phe	Arg	Lys	Lys	Glu	Met
321					645					650					655	
323	Lys	Asp	Tyr	Phe	Arg	Gln	Lys	Phe	Gln	Lys	Ile	Ala	Leu	Glu	Gly	Gly
324				660					665					670		
326	Gln	Tyr	Pro	Thr	Leu	Phe	Ser	Val	Leu	Glu	Asn	Glu	Gln	Asn	Asp	Leu
327			675					680					685			
329	Asn	Ala	Lys	Lys	Thr	Leu	Ile	Val	Glu	Ala	Lys	Gln	Arg	Asn	Tyr	Phe
330		690					695					700				
332	Lys	Lys	Asp	Asn	Leu	Leu	Gln	Pro	Val	Ile	Asn	Ile	Cys	Gln	Tyr	Asn
333		705				710					715					720
335	Tyr	Ile	Asn	Phe	Asn	Gly	Lys	Phe	Tyr	Lys	Gln	Thr	Lys	Gly	Ile	Pro
336					725					730					735	
338	Gln	Gly	Leu	Cys	Val	Ser	Ser	Ile	Leu	Ser	Ser	Phe	Tyr	Tyr	Ala	Thr
339				740					745					750		
341	Leu	Glu	Glu	Ser	Ser	Leu	Gly	Phe	Leu	Arg	Asp	Glu	Ser	Met	Asn	Pro
342			755					760					765			
344	Glu	Asn	Pro	Asn	Val	Asn	Leu	Leu	Met	Arg	Leu	Thr	Asp	Asp	Tyr	Leu
345		770					775					780				
347	Leu	Ile	Thr	Thr	Gln	Glu	Asn	Asn	Ala	Val	Leu	Phe	Ile	Glu	Lys	Leu
348		785				790					795					800
350	Ile	Asn	Val	Ser	Arg	Glu	Asn	Gly	Phe	Lys	Phe	Asn	Met	Lys	Lys	Leu
351					805					810					815	
353	Gln	Thr	Ser	Phe	Pro	Leu	Ser	Pro	Ser	Lys	Phe	Ala	Lys	Tyr	Gly	Met
354				820					825					830		
356	Asp	Ser	Val	Glu	Glu	Gln	Asn	Ile	Val	Gln	Asp	Tyr	Cys	Asp	Trp	Ile
357			835					840					845			
359	Gly	Ile	Ser	Ile	Asp	Met	Lys	Thr	Leu	Ala	Leu	Met	Pro	Asn	Ile	Asn
360		850					855					860				
362	Leu	Arg	Ile	Glu	Gly	Ile	Leu	Cys	Thr	Leu	Asn	Leu	Asn	Met	Gln	Thr
363		865				870					875					880
365	Lys	Lys	Ala	Ser	Met	Trp	Leu	Lys	Lys	Lys	Leu	Lys	Ser	Phe	Leu	Met
366					885					890					895	
368	Asn	Asn	Ile	Thr	His	Tyr	Phe	Arg	Lys	Thr	Ile	Thr	Thr	Glu	Asp	Phe
369				900					905					910		
371	Ala	Asn	Lys	Thr	Leu	Asn	Lys	Leu	Phe	Ile	Ser	Gly	Gly	Tyr	Lys	Tyr
372			915	</												

VERIFICATION SUMMARY

DATE: 02/07/2002

PATENT APPLICATION: US/10/054,611

TIME: 11:09:12

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Output Set: N:\CRF3\02072002\J054611.raw

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L:33 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
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Output Set: N:\CRF3\02072002\J054611.raw

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L:6624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6627 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6630 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
L:6639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174
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L:7324 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:202
L:7365 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7368 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:203
L:7490 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206
L:7743 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7746 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:7763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:216
L:7791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7833 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217
L:7908 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:217